

### **INPUT SET: S3895.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

## SEQUENCE LISTING

INPUT SET: S3895.raw

47 (C) STRANDEDNESS: single  
48 (D) TOPOLOGY: unknown  
49  
50 (ii) MOLECULE TYPE: peptide  
51  
52 (iii) HYPOTHETICAL: NO  
53  
54 (iv) ANTI-SENSE: NO  
55  
56 (vi) ORIGINAL SOURCE:  
57 (F) TISSUE TYPE: Bone  
58  
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
60  
61 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp  
62 1 5 10 15  
63  
64 Val Ile Ala Pro Gln Gly Tyr  
65 20  
66  
67 (2) INFORMATION FOR SEQ ID NO:2:  
68  
69 (i) SEQUENCE CHARACTERISTICS:  
70 (A) LENGTH: 18 amino acids  
71 (B) TYPE: amino acid  
72 (C) STRANDEDNESS: single  
73 (D) TOPOLOGY: unknown  
74  
75 (ii) MOLECULE TYPE: peptide  
76  
77 (iii) HYPOTHETICAL: NO  
78  
79 (iv) ANTI-SENSE: NO  
80  
81 (v) FRAGMENT TYPE: internal  
82  
83 (vi) ORIGINAL SOURCE:  
84 (A) ORGANISM: Bos taurus  
85 (F) TISSUE TYPE: Bone  
86  
87  
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
89  
90 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile  
91 1 5 10 15  
92  
93 Leu Arg  
94  
95  
96 (2) INFORMATION FOR SEQ ID NO:3:  
97  
98 (i) SEQUENCE CHARACTERISTICS:  
99 (A) LENGTH: 7 amino acids

INPUT SET: S3895.raw

100 (B) TYPE: amino acid  
101 (C) STRANDEDNESS: single  
102 (D) TOPOLOGY: unknown  
103  
104 (ii) MOLECULE TYPE: peptide  
105  
106 (iii) HYPOTHETICAL: NO  
107  
108 (iv) ANTI-SENSE: NO  
109  
110 (vi) ORIGINAL SOURCE:  
111 (A) ORGANISM: Bos taurus  
112 (F) TISSUE TYPE: Bone  
113  
114  
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
116  
117 Ala Cys Cys Ala Pro Thr Lys  
118 1 5  
119  
120 (2) INFORMATION FOR SEQ ID NO:4:  
121  
122 (i) SEQUENCE CHARACTERISTICS:  
123 (A) LENGTH: 23 amino acids  
124 (B) TYPE: amino acid  
125 (C) STRANDEDNESS: single  
126 (D) TOPOLOGY: unknown  
127  
128 (ii) MOLECULE TYPE: peptide  
129  
130 (iii) HYPOTHETICAL: NO  
131  
132 (vi) ORIGINAL SOURCE:  
133 (A) ORGANISM: Bos taurus  
134 (F) TISSUE TYPE: Bone  
135  
136  
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
138  
139 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp  
140 1 5 10 15  
141  
142 Val His Gly Ser His Gly Arg  
143 20  
144  
145 (2) INFORMATION FOR SEQ ID NO:5:  
146  
147 (i) SEQUENCE CHARACTERISTICS:  
148 (A) LENGTH: 80 base pairs  
149 (B) TYPE: nucleic acid  
150 (C) STRANDEDNESS: double  
151 (D) TOPOLOGY: linear  
152

INPUT SET: S3895.raw

153 (ii) MOLECULE TYPE: DNA (genomic)  
154  
155 (iii) HYPOTHETICAL: NO  
156  
157 (iv) ANTI-SENSE: NO  
158  
159 (vi) ORIGINAL SOURCE:  
160 (A) ORGANISM: Bos taurus  
161  
162 (vii) IMMEDIATE SOURCE:  
163 (B) CLONE: acc30  
164  
165 (viii) POSITION IN GENOME:  
166 (C) UNITS: bp  
167  
168 (ix) FEATURE:  
169 (A) NAME/KEY: CDS  
170 (B) LOCATION: 25..57  
171  
172  
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
174  
175 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51  
176 Lys Leu Ser Ala Thr Ser Val Leu Tyr  
177 1 5  
178  
179 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80  
180 Tyr Asp  
181 10  
182  
183  
184 (2) INFORMATION FOR SEQ ID NO:6:  
185  
186 (i) SEQUENCE CHARACTERISTICS:  
187 (A) LENGTH: 11 amino acids  
188 (B) TYPE: amino acid  
189 (D) TOPOLOGY: linear  
190  
191 (ii) MOLECULE TYPE: protein  
192  
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
194  
195 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp  
196 1 5 10  
197  
198 (2) INFORMATION FOR SEQ ID NO:7:  
199  
200 (i) SEQUENCE CHARACTERISTICS:  
201 (A) LENGTH: 199 base pairs  
202 (B) TYPE: nucleic acid  
203 (C) STRANDEDNESS: double  
204 (D) TOPOLOGY: linear  
205

INPUT SET: S3895.raw

206 (ii) MOLECULE TYPE: DNA (genomic)  
207  
208 (iii) HYPOTHETICAL: NO  
209  
210 (vi) ORIGINAL SOURCE:  
211 (A) ORGANISM: Bos taurus  
212  
213 (vii) IMMEDIATE SOURCE:  
214 (A) LIBRARY: Bovine genomic  
215 (B) CLONE: Lambda 9800-10  
216  
217 (viii) POSITION IN GENOME:  
218 (C) UNITS: bp  
219  
220 (ix) FEATURE:  
221 (A) NAME/KEY: exon  
222 (B) LOCATION: 30..199  
223  
224 (ix) FEATURE:  
225 (A) NAME/KEY: intron  
226 (B) LOCATION: 1..29  
227  
228 (ix) FEATURE:  
229 (A) NAME/KEY: CDS  
230 (B) LOCATION: 30..179  
231  
232  
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
234  
235 TGCCCCGCTGC CCCCTCCCGC CCCCGCCAG GTG CAC CTG CTG AAG CCG CAC GCG 53  
236 Val His Leu Leu Lys Pro His Ala  
237 1 5  
238  
239 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101  
240 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val  
241 10 15 20  
242  
243 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149  
244 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn  
245 25 30 35 40  
246  
247 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGGCCCCA ACTCCACCGG 196  
248 Met Val Val Arg Ala Cys Gly Cys His  
249 45 50  
250  
251 CAG 199  
252  
253  
254 (2) INFORMATION FOR SEQ ID NO:8:  
255  
256 (i) SEQUENCE CHARACTERISTICS:  
257 (A) LENGTH: 49 amino acids  
258 (B) TYPE: amino acid